1634

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RAW SEQUENCE LISTING
PATENT APPLICATION *US/08/939,905*

DATE: 05/26/98
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This Raw Listing contains the General
Information Section and up to the first 5 pages.

SEQUENCE LISTING ENTE

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 1
 2
 3   (1)      General Information:
 4
 5        (i) APPLICANT: GIJZEN, Mark
 6
 7       (ii) TITLE OF INVENTION:SEED COAT SPECIFIC DNA REGULATORY REGION
 8   AND PEROXIDASE
 9
10      (iii) NUMBER OF SEQUENCES: 2
11
12       (iv) CORRESPONDENCE ADDRESS:
13            (A) ADDRESSEE: NIXON & VANDERHYE P.C.
14            (B) STREET: 8th Floor, 1100 North Glebe Road
15            (C) CITY: Arlington
16            (D) STATE: Virginia
17            (E) COUNTRY: United States
18            (F) ZIP: 22201-4714
19
20        (v) COMPUTER READABLE FORM:
21            (A) MEDIUM TYPE: Floppy disk
22            (B) COMPUTER: IBM PC compatible
23            (C) OPERATING SYSTEM: PC-DOS/MS-DOS
24            (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
25
26       (vi) CURRENT APPLICATION DATA:
27            (A) APPLICATION NUMBER:
28            (B) FILING DATE: 26-SEP-1997
29            (C) CLASSIFICATION:
30
31      (vii) PRIOR APPLICATION DATA:
32            (A) APPLICATION NUMBER: US 08/723,414
33            (B) FILING DATE: 30-SEP-1996
34
35     (viii) ATTORNEY/AGENT INFORMATION:
36            (A) NAME: BYRNE, Thomas E.
37            (B) REGISTRATION NUMBER: 32,205
38            (C) REFERENCE/DOCKET NUMBER: 76-105
39
40       (ix) TELECOMMUNICATION INFORMATION:
41            (A) TELEPHONE: (703) 816-4021
42            (B) TELEFAX: (703) 816-4100
43
44
45   (2) INFORMATION FOR SEQ ID NO: 1:
46
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47          (i) SEQUENCE CHARACTERISTICS:
48               (A) LENGTH: 1244 base pairs
49               (B) TYPE: nucleic acid
50               (C) STRANDEDNESS: single
51               (D) TOPOLOGY: linear
52
53
54      (ii) MOLECULE TYPE: cDNA
55
56     (iii) HYPOTHETICAL: NO
57
58      (iv) ANTI-SENSE: NO
59
60
61      (ix) FEATURE:
62               (A) NAME/KEY: CDS
63               (B) LOCATION:1..1056
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65      (ix) FEATURE:
66               (A) NAME/KEY: sig_peptide
67               (B) LOCATION:1..77
68
69
70      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
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72   ATG GGT TCC ATG CGT CTA TTA GTA GTG GCA TTG TTG TGT GCA TTT GCT        48
73   Met Gly Ser Met Arg Leu Leu Val Val Ala Leu Leu Cys Ala Phe Ala
74    1           5                   10                  15
75
76   ATG CAT GCA GGT TTT TCA GTC TCT TAT GCT CAG CTT ACT CCT ACG TTC        96
77   Met His Ala Gly Phe Ser Val Ser Tyr Ala Gln Leu Thr Pro Thr Phe
78            20                  25                  30
79
80   TAC AGA GAA ACA TGT CCA AAT CTG TTC CCT ATT GTG TTT GGA GTA ATC       144
81   Tyr Arg Glu Thr Cys Pro Asn Leu Phe Pro Ile Val Phe Gly Val Ile
82        35                  40                  45
83
84   TTC GAT GCT TCT TTC ACC GAT CCC CGA ATC GGG GCC AGT CTC ATG AGG       192
85   Phe Asp Ala Ser Phe Thr Asp Pro Arg Ile Gly Ala Ser Leu Met Arg
86        50                  55                  60
87
88   CTT CAT TTT CAT GAT TGC TTT GTT CAA GGT TGT GAT GGA TCA GTT TTG       240
89   Leu His Phe His Asp Cys Phe Val Gln Gly Cys Asp Gly Ser Val Leu
90    65                  70                  75                  80
91
92   CTG AAC AAC ACT GAT ACA ATA GAA AGC GAG CAA GAT GCA CTT CCA AAT       288
93   Leu Asn Asn Thr Asp Thr Ile Glu Ser Glu Gln Asp Ala Leu Pro Asn
94                85                  90                  95
95
96   ATC AAC TCA ATA AGA GGA TTG GAC GTT GTC AAT GAC ATC AAG ACA GCG       336
97   Ile Asn Ser Ile Arg Gly Leu Asp Val Val Asn Asp Ile Lys Thr Ala
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99
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102            115             120             125
103
104    ATT GCA GCT GAA ATA GCT TCT GTT CTG GGA GGA GGT CCA GGA TGG CCA    432
105    Ile Ala Ala Glu Ile Ala Ser Val Leu Gly Gly Gly Pro Gly Trp Pro
106        130             135             140
107
108    GTT CCA TTA GGA AGA AGG GAC AGC TTA ACA GCA AAC CGA ACC CTT GCA    480
109    Val Pro Leu Gly Arg Arg Asp Ser Leu Thr Ala Asn Arg Thr Leu Ala
110    145             150             155             160
111
112    AAT CAA AAC CTT CCA GCA CCT TTC TTC AAC CTC ACT CAA CTT AAA GCT    528
113    Asn Gln Asn Leu Pro Ala Pro Phe Phe Asn Leu Thr Gln Leu Lys Ala
114                    165             170             175
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116    TCC TTT GCT GTT CAA GGT CTC AAC ACC CTT GAT TTA GTT ACA CTC TCA    576
117    Ser Phe Ala Val Gln Gly Leu Asn Thr Leu Asp Leu Val Thr Leu Ser
118                    180             185             190
119
120    GGT GGT CAT ACG TTT GGA AGA GCT CGG TGC AGT ACA TTC ATA AAC CGA    624
121    Gly Gly His Thr Phe Gly Arg Ala Arg Cys Ser Thr Phe Ile Asn Arg
122            195             200             205
123
124    TTA TAC AAC TTC AGC AAC ACT GGA AAC CCT GAT CCA ACT CTG AAC ACA    672
125    Leu Tyr Asn Phe Ser Asn Thr Gly Asn Pro Asp Pro Thr Leu Asn Thr
126        210             215             220
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128    ACA TAC TTA GAA GTA TTG CGT GCA AGA TGC CCC CAG AAT GCA ACT GGG    720
129    Thr Tyr Leu Glu Val Leu Arg Ala Arg Cys Pro Gln Asn Ala Thr Gly
130    225             230             235             240
131
132    GAT AAC CTC ACC AAT TTG GAC CTG AGC ACA CCT GAT CAA TTT GAC AAC    768
133    Asp Asn Leu Thr Asn Leu Asp Leu Ser Thr Pro Asp Gln Phe Asp Asn
134                    245             250             255
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136    AGA TAC TAC TCC AAT CTT CTG CAG CTC AAT GGC TTA CTT CAG AGT GAC    816
137    Arg Tyr Tyr Ser Asn Leu Leu Gln Leu Asn Gly Leu Leu Gln Ser Asp
138                260             265             270
139
140    CAA GAA CTT TTC TCC ACT CCT GGT GCT GAT ACC ATT CCC ATT GTC AAT    864
141    Gln Glu Leu Phe Ser Thr Pro Gly Ala Asp Thr Ile Pro Ile Val Asn
142                275             280             285
143
144    AGC TTC AGC AGT AAC CAG AAT ACT TTC TTT TCC AAC TTT AGA GTT TCA    912
145    Ser Phe Ser Ser Asn Gln Asn Thr Phe Phe Ser Asn Phe Arg Val Ser
146        290             295             300
147
148    ATG ATA AAA ATG GGT AAT ATT GGA GTG CTG ACT GGG GAT GAA GGA GAA    960
149    Met Ile Lys Met Gly Asn Ile Gly Val Leu Thr Gly Asp Glu Gly Glu
150    305             310             315             320
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152    ATT CGC TTG CAA TGT AAT TTT GTG AAT GGA GAC TCG TTT GGA TTA GCT    1008
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153   Ile Arg Leu Gln Cys Asn Phe Val Asn Gly Asp Ser Phe Gly Leu Ala
154                   325               330               335
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156   AGT GTG GCG TCC AAA GAT GCT AAA CAA AAG CTT GTT GCT CAA TCT AAA      1056
157   Ser Val Ala Ser Lys Asp Ala Lys Gln Lys Leu Val Ala Gln Ser Lys
158                   340               345               350
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160   TAAACCAATA ATTAATGGGG ATGTGCATGC TAGCTAGCAT GTAAAGGCAA ATTAGGTTGT    1116
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162   AAACCTCTTT GCTAGCTATA TTGAAATAAA CCAAAGGAGT AGTGTGCATG TCAATTCGAT    1176
163
164   TTTGCCATGT ACCTCTTGGA ATATTATGTA ATAATTATTT GAATCTCTTT AAGGTACTTA    1236
165                                                                       1244
166   ATTAATCA
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168
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170   (2) INFORMATION FOR SEQ ID NO: 2:
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172           (i) SEQUENCE CHARACTERISTICS:
173                   (A) LENGTH: 4700 base pairs
174                   (B) TYPE: nucleic acid
175                   (C) STRANDEDNESS: single
176                   (D) TOPOLOGY: linear
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178           (ii) MOLECULE TYPE: DNA (genomic)
179
180
181           (ix) FEATURE:
182                   (A) NAME/KEY: promoter
183                   (B) LOCATION:1..1532
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185           (ix) FEATURE:
186                   (A) NAME/KEY: sig_peptide
187                   (B) LOCATION:1533..1609
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190                   (A) NAME/KEY: exon
191                   (B) LOCATION:1533..1751
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195                   (B) LOCATION:2383..2574
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201           (ix) FEATURE:
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203                   (B) LOCATION:4033..4516
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205           (ix) FEATURE:
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206                (A) NAME/KEY: intron
207                (B) LOCATION:1752..1782
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211                (B) LOCATION:2575..3604
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215                (B) LOCATION:3770..4032
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217      (ix) FEATURE:
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219                (B) LOCATION:1533..1751
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227                (B) LOCATION:3605..3769
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229      (ix) FEATURE:
230                (A) NAME/KEY: CDS
231                (B) LOCATION:4033..4516
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234      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
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236   TAGATAAAAA AATGGGATAT AATTTTTCTC AGATGTTGTT TATACTGTTT TTTTAATCAG    60
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238   AATTAAAATT CCTCTTTAAT TATCGACATA ATTTTTTTTG GTGAATATTA TCGACATAAT   120
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240   TATTTAATAC AAATTTTTAT TGTACATAGA AGTGATACTT CAATTTTAAT ATTGGAGAAC   180
241
242   AGTACGAAAA CATAAAAAAA CTGTTATTAG AAGAAAAAAA TATATGGAAA AGGTTAGCTA   240
243
244   CATATATTAG CTAAATTAGT TGTTCTAATT GGCTATATAA ACCCTATTGT ACTCTTTGTA   300
245
246   ATCTCACCTT TTTCATTTAA ATACATTTCT ACTTTTTAAG TTCTATATTT TCTCTCAATT   360
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248   TTCTTCGATA AACCATGAAA TTTAACATGG TATATCAGCG ATACCACCCA CTTTGAAAGC   420
249
250   CATGTATGGC TAGTATGGGC AGCCAAAATT TGCCCTGGTT CAAGCAAAGC AAGTGTTTAT   480
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252   ATAGATGTGA CTTTTGTTGA GGAACTCATG CCAATGGTAC TGATTGTGAA ACTGAGAAAA   540
253
254   CTAATTTGGA GAATTTGAAT TATGATCATT AAATACTCCT CTCCTGACTA CCTTCGTCCC   600
255
256   TCAAATTTGT ACCATCATTA TTTCCCAAAA ATTTGATTAC AATGCACTAA TTAATGAATG   660
257
258   TTTCTTACAT TATCATATTA TCATATCTGA CATTTTGTTT TTACTTTTTA TAATAATTAT   720
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SEQUENCE VERIFICATION REPORT
PATENT APPLICATION   *US/08/939,905*

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